In the Claims

Claims 1-30 (Canceled).

Claim 31 (New): A transformed host cell that comprises one or more genetic construct that comprises SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO:3.

Claim 32 (New): The transformed host cell of claim 31, wherein said transformed host cell has been transformed with multiple genetic constructs.

Claim 33 (New): The transformed host cell of claim 2, wherein said multiple genetic constructs contain SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO: 3, polynucleotide fragments of SEQ ID NOs: 1-3, or combinations of polynucleotide fragments of SEQ ID NOs 1-3.

Claim 34 (New): The transformed host cell of claim 31, wherein said host cell has been transformed with one or more genetic constructs that provide a combination of polynucleotide fragments of SEQ ID NOs: 1, 2, and 3, wherein said combination of polynucleotide fragments provide a biosynthetic pathway for the production of albicidin or an albicidin-like antibiotic.

Claim 35 (New): A method of making an antibiotic comprising the culturing of a transformed host cell according to claim 31 under conditions that allow for the production of said antibiotic.

Claim 36 (New): The method according to claim 6, further comprising the isolation of said antibiotic.

Claim 37 (New): A composition of matter comprising:

(a) an isolated polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(b) an isolated polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(c) an isolated polynucleotide that is complementary to a polynucleotide selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(d) an isolated polynucleotide that is complementary to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; or

(e) an isolated polynucleotide that is at least 70% homologous to: (1) a polynucleotide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25; (2) a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; (3) a polynucleotide that is complementary to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; (3) a polynucleotide that is complementary to a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, and 25;

(f) an isolated polynucleotide sequence encoding a variant of a polypeptide selected from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said variant has at least one of the biological activities associated with the polypeptides of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

g) an isolated polynucleotide sequence encoding a fragment of a polypeptide selected from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47 or a fragment of a variant polypeptide of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

h) an isolated polynucleotide sequence encoding multimeric construct comprising a polynucleotide as set forth in (a), (b), (c), (d), (e), (f), or (g);

(i) an isolated polynucleotide that hybridizes under low, intermediate or high stringency with a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h);

j) a genetic construct comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), or (i);

k) a vector comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), or (i);

(l) a promoter operably linked to a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), or (i);

(m) a recombinant cell comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k) or (l);

(n) an isolated polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(o) a heterologous polypeptide sequence fused, in frame, to a polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(p) a polypeptide fragment of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said fragment exhibits at least one biological function of the polypeptide of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(q) a variant polypeptide having at least 70% homology to a polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said variant exhibits at least one biological function of the polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(r) an isolated purified antibiotic having at least 4 of the structural elements illustrated in Figure 11, and an elemental composition of $C_{40}H_{35}N_6O_{15}$;

(s) an isolated and purified antibiotic produced by a process that includes at least three proteins coded by DNA sequences of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k) or (l) in combination with additional enzymes that modify the product to provide a non-naturally occurring

Albicidin-like product having at least one of the useful properties reported for albicidin;

(t) an antibiotic or antibiotics having at least one of the general structures illustrated in Figure 11;

(u) an antibiotic produced by the process of expressing the DNA of one or more of the genes included in the Albicidin Biosynthetic Gene Clusters in a genetically modified host cell sustained in a culture media, and thereafter separating the antibiotic from the host cell and culture media; or

(v) a genetic construct comprising at least one polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 3.

Claim 38 (New): The recombinant cell of claim 37, wherein said cell has been transformed with at least one polynucleotide sequence comprising SEQ ID NO: 1, 2, or 3.

Claim 39 (New): The recombinant cell of claim 38, wherein said cell has been transformed with at least two of said polynucleotide sequences.

Claim 40 (New): The recombinant cell of claim 38, wherein said cell has been transformed with SEQ ID NO: 1, SEQ ID NO: 2 and SEQ ID NO: 3.

Claim 41 (New): A method of using a composition of matter according to claim 37 for the production of a protein, for the production of a polyketide carrying para-aminobenzoic acid, for activating non-proteinogenic amino acids for incorporation into peptides or polyketides, for producing an antibiotic, for protecting a plant against damage from albicidin, for obtaining agents useful in blocking expression of albicidin, or for protecting a plant against phytotoxic damage from an antibiotic.

Claim 42 (New): The method of claim 41, wherein said method comprises producing a protein comprising the steps of expressing a polynucleotide according to claim 37 in a host cell under conditions that allow for the expression of said polynucleotide.

Claim 43 (New): The method according to claim 42, further comprising the isolation of said protein.

Claim 44 (New): The method according to claim 41, wherein said method comrpises producing a polyketide carrying para-aminobenzoic acid and/or carbamoyl benzoic acid by inserting at least one DNA Fragment of claim 37 that encodes a polyketide synthetase (PKS) into a cell and causing the cell to express the encoded PKS protein under conditions such that the PKS functions to produce a polyketide carrying either a para-aminobenzoic acid or a carbamoyl benzoic acid or both.

Claim 45 (New): The method according to claim 41, wherein said method comprises activating non-proteinogenic amino acids for incorporation into peptides or polyketides by inserting at least one DNA Fragment of Claim 37 that encodes a polyketide synthetase (PKS) into a cell and causing the cell to express the encoded PKS under conditions such that the PKS activates said non-proteinogenic amino acids.

Claim 46 (New): The method according to claim 45, wherein said non-proteinogenic amino acids are para-aminobenzoic acid or carbamoyl benzoic acid.

Claim 47 (New): The method according to claim 41, wherein said method comprises modifying a host cell to enhance expression of a polynucleotide according to claim 37 comprising the insertion of expression enhancing DNA into the genome of a Xanthomonas albilineans strain, Escherichia coli strain, or other Albicidin producing microbial strain, in a position operative to enhance expression of the enzymes of the Albicidin Biosynthetic Gene Clusters, culturing the modified host cell to produce an antibiotic and isolating the antibiotic.

Claim 48 (New): The method according to claim 41, wherein said method comprises protecting a plant against damage from albicidin that comprises applying an agent that blocks expression at least one gene in the Albicidin Biosynthetic Gene Clusters to the plant to be protected.

Claim 49 (New): The method according to claim 41, wherein said method comprises obtaining agents useful in blocking expression of albicidin by screening materials against a modified host cell line that expresses a polynucleotide according to claim 37 and selecting for materials that stop or decrease albicidin production.

Claim 50 (New): The method according to claim 41, wherein said method comprises protecting a plant against phytotoxic damage from an antibiotic that comprises inserting into the plant and operably expressing at least one resistance gene from the polynucleotides according to claim 37 in the plant to be protected.